

Cyr61	M--SSSTFRTLAVAVTLHL--TRLALST-CPAAG--HCPLF-AFKCAPGVGLVFDGCGGCKVCK	58
CEP10	M--GSAGARP-ALAAALLCL--ARIALGSPCPAVC--QCPAA-AFQCAPGVGLVFDGCGGCKVCK	58
Fisp12	M--LASVAGPISLA-LVLLALCTRPATQDCSAQC--QCAAEAAFPKCPAGVSLFLDGGCGGCKVCK	61
CTGF	M--TAASNGPVRVAFVVLALCSRPAVQONCSGFC--RCFDEPAPRCPAGVSLFLDGGCGGCKVCK	62
Nov	NETGGCGGLFVLLILLILRPFCEVSGREAACPRFCGGCTAEP-PRCAPGVPAVLGGCGGCKVCK	65
Cyr61	QLNEDCSKTQPCDHTKGLCNFGASSTALNGICRAQSEGRPCFYNSKIYONGESFPNCHQCTCI	124
CEP10	QLNEDCSRTOEDHTKGLCNFGASPAATNGICRAQSEGRPCFYNSKIYONGESFPNCHQCTCI	124
Fisp12	QLGELCTERDECDPHKGLFCDFGSPANRKIGVCTAK-DGAPGVFGGSVRSGETSSICKYQCTEL	126
CTGF	QLGELCTERDECDPHKGLFCDFGSPANRKIGVCTAK-DGAPGVFGGSVRSGETSSICKYQCTEL	127
Nov	QRGESCSPLPCDESGLCYDRGPEDCGGAGLGVNL-EDNGVFDGCGGCKVCKETEPSSICKYQCTEL	130
Cyr61	DGAVGCIPLCPQELSLPMLGCPNPRLVKVSQCCEEVVCDSDSIK-DSLDD-QDDLLGLDASEVEL	188
CEP10	DGAVGCIPLCPQELSLPMLGCPNPRLVKVSQCCEEVVCDSDSIK-DSLDD-QDDLLGLDASEVEL	190
Fisp12	DGAVGCVPLCSMDVRLPSPDGPFPRVKLPKCCCEEVVCDPEKDKIAVGP-----ALAKYRLSD	185
CTGF	DGAVGCVPLCSMDVRLPSPDGPFPRVKLPKCCCEEVVCDPEKDKIAVGP-----ALAKYRLSD	186
Nov	DQIGICLFRNLGLLLCPDGPFPFKIEVPGECCCEEVVCDPRDEVLLGGF-----AMAKYRQEA	189
Cyr61	TRNNELIAIGKSSSLQRLPVFCTEPRVLFNPLHAGQKCTVQTTSSSQCSKSGGTGISDRVDRHTP	254
CEP10	TRNNELIAIVKGG-LQQLPVFCSEPO-----SRAFENPKCTVQTTSSSQCSKSGGTGISDRVDRHTP	251
Fisp12	T-----FGFDP-----TMRANCLVQTTENSACSKECTGGTISDRVDRHTP	225
CTGF	T-----FGFDP-----TMRANCLVQTTENSACSKECTGGTISDRVDRHTP	226
Nov	T-----LGI DV-----SDSSANGTEQTTENSACSKECTGGTISDRVDRHTP	229
Cyr61	ECRLVKETKICEVRPCGQPVYSLSLQGGKCKCTKCKSPFVRFTYAGSSVQCCRPKYDGSQVDRGK	320
CEP10	DCRLVKETKICEVRPCGQPSYASLSLQGGKCKCTKCKSPFVRFTYAGSSVQCCRPKYDGSQVDRGK	317
Fisp12	FORLEKQSRLENVRPCDADLEENTLQGGKCTKCTKCLAKPVKFELSGETSVKCTRAKFGGCTDGRD	291
CTGF	SCRLEKQSRLENVRPCDADLEENTLQGGKCTKCTKCLAKPVKFELSGETSVKCTRAKFGGCTDGRD	292
Nov	QCEMVKQTRLENVRPCEN-EFSDKQGGKCTKCTKCLAKPVKFELSGETSVKCTRAKFGGCTDGRD	294
Cyr61	CTFLQTKTVQKFRCEGDEGTSIONVM-IOCKQNYNCNPHREASTRLY--SLFRDIHCKFRD	379
CEP10	CTFQTKTVQKFRCEGDEGTSIONVM-IOCKQNYNCNPHREASTRLY--SLFRDIHCKFRD	376
Fisp12	CTFRLTTLFVEFKCPDGEVMQON-HGDKTCAHYNCPCDRDI FESLYYRKYGDMA	348
CTGF	CTFRLTTLFVEFKCPDGEVMQON-HGDKTCAHYNCPCDRDI FESLYYRKYGDMA	349
Nov	CTFHNDCIIVQFRCPQGGFLQCP-HGLINTCVCHNCPCQSHNAFTQPLDPMSSSEAKI	351

FIGURE 1

2022T0"ES4ES00T

CYR61
CEF10
FISP12
CTGF
Nov

M--SSSTFRTLAVAVTLLHL--TRLALST-CPAAC--HCPLE-APKCAPGVGLVRDGGCGCKKVCAC
M--GSAGARP-ALAAALLCL--ARLALGSPCAVC--QCPAA-APQCAPGVGLVPDGGCGCKKVCAC
M--LASVAGPISLA-LVLLALCTRPATGQDCSAQC--QCAAEAAHPCAPGVSLVLDGGCGCCRVCAC
M--TAASMGVPRVAFVLLALCSRPAVGQNCSPC--RCPDEPAPRCAPGVSLVLDGGCGCCRVCAC
METGGGQGLPVLLLLLLLRPCEVSGREACPRPCGGRCPAEP-PRCAPGVPAVLDGGCGCCLVCAR

58
58
61
62
65

CYR61
CEF10
FISP12
CTGF
Nov

QLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCCEYNSRIYONGESFQPNCKHQCTCI
QLNEDCSRTQPCDHTKGLECNFGASPAATNGICRAQSEGRPCCEYNSKIYONGESFQPNCKHQCTCI
QLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGGSVYRSGESFQSSCKYQCTCL
QLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCIFGGTVYRSGESFQSSCKYQCTCL
ORGESCSPLLPCEDESGGLYCDRGPEDGGGAGICMVL-EGDNCVFDGMIYRNGETFPSPCKYQCTCR

124
124
126
127
130

CYR61
CEF10
FISP12
CTGF
Nov

DGAVGCIPLCPOELSLPNLGCNPRLVKVSGQCCCEEWVCEDESIK-DSLDD-QDDLGLDASEVEL
DGAVGCIPLCPOELSLPNLGCPSRRLVKVPGQCCCEEWVCEDESKDALEELEGFFSKEFGLDASEGEL
DGAVGCVPLCSMDVRLSPDCPFPRRVKLPKCKCKEWVCEDEPKDRTAVGP-----ALAAAYRLED
DGAVGCMPLCSMDVRLSPDCPFPRRVKLPKCKCEEWVCEDEPKDQTVVGP-----ALAAAYRLED
DGOIGCLPRCNLGLLLPGPDPCPFPRKIEVPGECKWVCDPRDEVLLGGF-----AMAAAYRQEA

188
190
185
186
189

FIGURE 1 (1 of 2)

202210" E9/ES001

CYR61 TRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIQVTTWSQCSKSCGTGISTRVTNDNP 254
 CEF10 TRNNELIAIVKGG-LKMLPVFGSEPO-----SRAFENPKCIVQTTWSQCSKTCGTGISTRVTNDNP 251
 FISP12 T-----FGPDP-----TMMRANCLVQTTESACSKTCGMGISTRVTNDNT 225
 CTGF T-----FGPDP-----TMIRANCLVQTTESACSKTCGMGISTRVTNDNA 226
 NOV T-----LGIDV-----SDSSANCIEQTTESACSKSCGMGFSTRVTNRNQ 229

CYR61 ECRLVKETRICEVRPCGQPVYSSLKGGKKCKTKKSPVRFITYAGCSSVKKYRPHYCGSCVDGRC 320
 CEF10 DCKLIKETRICEVRPCGQPSYASLKGGKKCTKTKSPVRFITYAGCSSVKKYRPHYCGSCVDGRC 317
 FISP12 FCRLEKQSRLCMVRPCEADLEENIKGGKKCIRTPKIAKPVKFELSGCTSVKTYRAKFCGVCTDGRC 291
 CTGF SCRLEKQSRLCMVRPCEADLEENIKGGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRC 292
 NOV QCCEMVKQTRLCHMRPCEN-EEPSDKGGKKCIQTKKSMKAVRFEYKNCTSVQTYKPRYCGLCNDGRC 294

CYR61 CTPLQTRTVKMRFCEDGEMFSKNVMM-IQSCCKNYNCNCPHPNEASFRLY--SLFNDIHKFRD 379
 CEF10 CTPQQTTRTVKIRFCDDGETFTKSVM--IQSCRCNYNCNCPHANE--YPFY--RLVNDIHKFRD 376
 FISP12 CTPHRTTTLTPVEFKCPDGEIMKN--MMFIKTCACHYNCPGNDIFESLYRKMVGMDA 348
 CTGF CTPHRTTTLTPVEFKCPDGEVMKN--MMFIKTCACHYNCPGNDIFESLYRKMVGMDA 349
 NOV CTPHNTKTIQVEFRCPQKFLKKP--MMLINTCVCHGNCPOSNAFFQPLDPMSEAKI 351

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FIGURE 1 (2 of 2)